

SEQUENCE LISTING

<110> TAKASHIMA, Shou
TSUJIMOTO, Masafumi
TSUJI, Shuichi

<120> GLYCOSYLATING ENZYME

<130> P25687

<140> US 10/501,930

<141> 2004-07-29

<150> PCT/JP03/00883

<151> 2003-01-30

<160> 30

<170> PatentIn version 3.3

<210> 1

<211> 398

<212> PRT

<213> Mouse

<400> 1

Met Arg Ser Gly Gly Thr Leu Phe Ala Leu Ile Gly Ser Leu Met Leu
1 5 10 15

Leu Leu Leu Leu Arg Met Leu Trp Cys Pro Ala Asp Ala Pro Ala Arg
20 25 30

Ser Arg Leu Leu Met Glu Gly Ser Arg Glu Asp Thr Ser Gly Thr Ser
35 40 45

Ala Ala Leu Lys Thr Leu Trp Ser Pro Thr Thr Pro Val Pro Arg Thr
50 55 60

Arg Asn Ser Thr Tyr Leu Asp Glu Lys Thr Thr Gln Ile Thr Glu Lys
65 70 75 80

Cys Lys Asp Leu Gln Tyr Ser Leu Asn Ser Leu Ser Asn Lys Thr Arg
85 90 95

Arg Tyr Ser Glu Asp Asp Tyr Leu Gln Thr Ile Thr Asn Ile Gln Arg
100 105 110

Cys Pro Trp Asn Arg Gln Ala Glu Glu Tyr Asp Asn Phe Arg Ala Lys
115 120 125

Leu Ala Ser Cys Cys Asp Ala Ile Gln Asp Phe Val Val Ser Gln Asn
130 135 140

Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys
145 150 155 160

His Ile Pro Ile Arg Glu Asn Ile Phe His Met Phe Pro Val Ser Gln
165 170 175

Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly
180 185 190

Gly Ile Leu Asn Lys Ser Leu Cys Gly Ala Glu Ile Asp Lys Ser Asp
195 200 205

Phe Val Phe Arg Cys Asn Leu Pro Pro Ile Thr Gly Ser Ala Ser Lys
210 215 220

Asp Val Gly Ser Lys Thr Asn Leu Val Thr Val Asn Pro Ser Ile Ile
225 230 235 240

Thr Leu Lys Tyr Gln Asn Leu Lys Glu Lys Lys Ala Gln Phe Leu Glu
245 250 255

Asp Ile Ser Thr Tyr Gly Asp Ala Phe Leu Leu Leu Pro Ala Phe Ser
260 265 270

Tyr Arg Ala Asn Thr Gly Ile Ser Phe Lys Val Tyr Gln Thr Leu Lys
275 280 285

Glu Ser Lys Met Arg Gln Lys Val Leu Phe Phe His Pro Arg Tyr Leu
 290 295 300

Arg His Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg
 305 310 315 320

Leu Ser Thr Gly Leu Met Ile Ala Ser Val Ala Val Glu Leu Cys Glu
 325 330 335

Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Ile Glu Asp
 340 345 350

Thr Pro Leu Ser His His Tyr Tyr Asp Asn Met Leu Pro Lys His Gly
 355 360 365

Phe His Gln Met Pro Lys Glu Tyr Ser Gln Met Leu Gln Leu His Met
 370 375 380

Arg Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Thr Ala
 385 390 395

<210> 2
 <211> 3166
 <212> DNA
 <213> Mouse

<400> 2						
cgagcgcccg	agtcggtgcc	gcccgggctg	cgttcgccc	cggcagctt	ggcgccgagg	60
acgcccgtgg	ctcaggatga	gatcgaaaaa	cacgctgttc	gccctcatag	gcagcctgat	120
gctgctgctc	ctcctgcgt	tgctctggtg	cccagccgac	gcccctgccc	gctccaggct	180
gttcatggag	ggaaggcagag	aggacaccag	ttgtaccta	gctgcactga	agacactctg	240
gagcccgaca	accgggtac	cacgcaccag	gaacagcaca	tatctggatg	agaagacaac	300
ccaaataaca	gagaaatgca	aagatctgca	atatacgat	aactctttat	ctaacaaaac	360
gagacggta	tctgaggatg	actacactcca	gaccatcaca	aacatacaga	gatgccatg	420

gaaccggcaa	gcagaagaat	atgacaattt	tagagcaaaa	ctggcttcct	gttgcgatgc	480
cattcaagac	ttcgtggttt	cccagaacaa	caactccagtg	gggactaaca	ttagctacga	540
ggtggaaagc	aagaaacaca	tccccattcg	agagaacatt	ttccacatgt	ttccagtgtc	600
gcagcccttt	gtggactatc	cctataacca	gtgtcagtg	gttggtaatg	gggaaattct	660
caacaagtct	ctctgcggag	cagaaattga	taaatctgac	ttcgtcttca	ggtgtaacct	720
ccccccaatc	acagggagcg	ctagtaaaga	tgttggaaagc	aaaacaaatc	ttgtgactgt	780
caatcccagc	attataaccc	tgaagtacca	gaatttgaag	gagaagaaaag	cacagtttt	840
ggaggacatc	tccacctatg	gagatgcatt	cctcctcctg	ccagcatttt	cctatcgggc	900
caacacaggc	atctctttta	aagtctacca	aacactcaaa	gagtcaaaaa	tgaggcaaaa	960
ggttctcttc	ttccatccca	ggtacctgag	acacctcgct	ctttctgga	gaactaaagg	1020
ggtgactgca	taccgcttgt	ccacaggctt	gatgattgca	agtgtcgctg	tggaactgtg	1080
tgaaaacgtg	aagctctacg	gattctggcc	tttctctaag	actatcgaag	acaccccact	1140
cagtcaccac	tactatgata	acatgttacc	taagcatgg	ttccaccaga	tgcctaaaga	1200
atacagccaa	atgctccagc	tccatatgag	aggaatcctc	aaactgcaat	tcagcaaatg	1260
tgaaacggct	taacgtttct	tagaaggaga	ataatttcag	gaggtggagt	ggatgtgtca	1320
cagcatctcc	aaaaagccaa	tagaagaagg	cacagagaaa	gcatgaatta	caaaggcgct	1380
ctcccacttg	tctagaccaa	agccacccgc	ccccactcac	tttgcagcct	ccacgagtca	1440
ctcattctca	ccttcaacgt	tctttctctg	agaatagaga	ccaaaacatc	agacttggat	1500
aagtaaaatg	agataatttt	tcaaatcatc	atagaatttg	atttgagcca	gggtctctca	1560
gaatgcttcc	ttgttcctat	ccatgatagc	cattcccacc	tttatcagag	tggtaatgaa	1620
actgtgcaat	tgtgccaaag	acccttctg	aagagaatgt	ctgaatcatg	cggcgagtt	1680
ttacacacag	ctcttccttt	ataaataaaat	ccttcccatt	ctccctccta	gtagagtaca	1740
gaaacaaaat	acccttgatg	attcaggaag	aaaagtcttt	tttacttagc	aatgtgcctg	1800
cttctgattc	agttcgcttg	tgacattaag	ctgggttggg	gttttgggtt	gatttggggc	1860
gtttcttcac	ttctttgtc	tatatttcc	ttacctttag	cagtttgtat	tcgagcttcc	1920

tgctttggga ttctgcaatt ctctctccca ctgacaggat caactcaatg acataaaagta	1980
gttcaaacat ccattgcttc tcacatgttt tatccataaa gttactcatc tgattttatt	2040
taaaatagtg aacatctact tgatatcaga cccgaggacc atcctccatt ggagaatatg	2100
aagatattgt cactggcaga aaagcaggtg tgtgccatta attgataaga taccacaagc	2160
atcatcatgc cagttatgaa cacagtgctg aaaggatcat agacaggggt ggttaaatct	2220
gatcccagta gaataaaactt cagtgtacct atttcaggga agagttaatt tcacaattaa	2280
aactagtaaa tgaaccaatt cttaggcaca ttaagtggat tctgagtaaa agaaaggaa	2340
cagcaggaga aagctgttcg cttgggtctg attacccaaa tgagcatgct ggaaggaggt	2400
tgtgaggcta cgctaaaacc tctgcgtagg gagagagtagc agtgcattgag tgtggcggct	2460
tttgtccaca ctcgtgaagg gtgagtaatt cagagccaat cacatcacaac ggtatggacac	2520
acctaactca tcacttcagg gggagatgaa tgctttcatg agaaattaca ctcataagct	2580
aagcatcagt tttgagtaaa atttgagtag atgttaataa tgaacatttt atacctctta	2640
ctaatgtccc accgacacact tttaatgtaa gcacatttat ttattaagtt acttgacatt	2700
aaatgcttat gtctgtatat tctgttcatc catcgatttt cccaaaaagt aagagcatag	2760
gagatgaggc ctacatgcc aaaaaactat aaattttact ctttaattct tacttgagcc	2820
agcttgggtt ttatcaagtg ctttttgaa gagacagcac cctgtgaatt cttcattctg	2880
atacagtgtc accttgttatt taacatttgt aatgttggtt caagttaca tctctttcat	2940
tctttatag caaatcaaac gtattagctt cagaaattta tcagaagttc atatataaaat	3000
attttgcaaa gggtaaaagg ctttttggtt aaataaaata aaatttattt ttttcttctg	3060
atgaatagag gctctttat gctgctgcta atgaacctaa ttagctttaa attatctcct	3120
agcaacattg gtcacgttc aatcatgcta ttagcaaaaa aaaaaa	3166

<210> 3
 <211> 398
 <212> PRT
 <213> Human

<400> 3

Met Arg Pro Gly Gly Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Arg Leu Leu Trp Cys Pro Ala Asp Ala Pro Gly Arg
20 25 30

Ala Arg Ile Leu Val Glu Glu Ser Arg Glu Ala Thr His Gly Thr Pro
35 40 45

Ala Ala Leu Arg Thr Leu Arg Ser Pro Ala Thr Ala Val Pro Arg Ala
50 55 60

Thr Asn Ser Thr Tyr Leu Asn Glu Lys Ser Leu Gln Leu Thr Glu Lys
65 70 75 80

Cys Lys Asn Leu Gln Tyr Gly Ile Glu Ser Phe Ser Asn Lys Thr Lys
85 90 95

Gly Tyr Ser Glu Asn Asp Tyr Leu Gln Ile Ile Thr Asp Ile Gln Ser
100 105 110

Cys Pro Trp Lys Arg Gln Ala Glu Glu Tyr Ala Asn Phe Arg Ala Lys
115 120 125

Leu Ala Ser Cys Cys Asp Ala Val Gln Asn Phe Val Val Ser Gln Asn
130 135 140

Asn Thr Pro Val Gly Thr Asn Met Ser Tyr Glu Val Glu Ser Lys Lys
145 150 155 160

Glu Ile Pro Ile Lys Lys Asn Ile Phe His Met Phe Pro Val Ser Gln
165 170 175

Pro Phe Val Asp Tyr Pro Tyr Asn Gln Cys Ala Val Val Gly Asn Gly
180 185 190

Gly Ile Leu Asn Lys Ser Leu Cys Gly Thr Glu Ile Asp Lys Ser Asp
195 200 205

Phe Val Phe Arg Cys Asn Leu Pro Pro Thr Thr Gly Asp Val Ser Lys
210 215 220

Asp Val Gly Ser Lys Thr Asn Leu Val Thr Ile Asn Pro Ser Ile Ile
225 230 235 240

Thr Leu Lys Tyr Gly Asn Leu Lys Glu Lys Lys Ala Leu Phe Leu Glu
245 250 255

Asp Ile Ala Thr Tyr Gly Asp Ala Phe Phe Phe Leu Pro Ala Phe Ser
260 265 270

Phe Arg Ala Asn Thr Gly Thr Ser Phe Lys Val Tyr Tyr Thr Leu Glu
275 280 285

Glu Ser Lys Ala Arg Gln Lys Val Leu Phe Phe His Pro Lys Tyr Leu
290 295 300

Lys Asp Leu Ala Leu Phe Trp Arg Thr Lys Gly Val Thr Ala Tyr Arg
305 310 315 320

Leu Ser Thr Gly Leu Met Ile Thr Ser Val Ala Val Glu Leu Cys Lys
325 330 335

Asn Val Lys Leu Tyr Gly Phe Trp Pro Phe Ser Lys Thr Val Glu Asp
340 345 350

Ile Pro Val Ser His His Tyr Tyr Asp Asn Lys Leu Pro Lys His Gly
355 360 365

Phe His Gln Met Pro Lys Glu Tyr Ser Gln Ile Leu Gln Leu His Met
370 375 380

Lys Gly Ile Leu Lys Leu Gln Phe Ser Lys Cys Glu Val Ala
 385 390 395

<210> 4
 <211> 1500
 <212> DNA
 <213> Human

<400> 4
 ggtggcggcg gcggcgggag ccgcgagtcg gggccgcccgg ggttgtgctt cgcggcggca 60
 gcagcggtgg cggcgccgc tggctcag gatgcggccg gggggcgcac tgctcgccct 120
 gctcgccagc ctgctgctgc tgctgctgct ggcctgctc tggtgcccg cagacgcgcc 180
 cggccgcgc aggattctgg tggaggaaag cagggaggcc acccacggca ccccccgcagc 240
 gctgaggacg ctccggagcc cggcgaccgc ggtaccgcgc gccactaaca gcacatatct 300
 gaatgagaag tcgctccaac tgacggagaa atgaaaaat ctgcaatatg gcattgagtc 360
 tttctctaac aaaacgaaag ggtattcaga gaacgactac cttcagatta tcacagat 420
 acagagttgt ccatggaaac ggcaagcaga agaatatgca aatttttagag ccaaacttgc 480
 ttcctgctgt gatgctgttc aaaactttgt tggctcag aataacactc cagttggac 540
 taatatgagt tacgaggtgg aaagaaaaa agaaatccca attaagaaga acattttca 600
 tatgtttcca gtgtcccagc cttttgtgga ctacccttat aatcagtgtg cagtggtcgg 660
 aaatggggaa attctgaata agtctctctg tggactgaa atagataaat ccgacttcgt 720
 ttttaggtgt aacctacccc caaccacagg agatgttagt aaagatgttgc gcagtaaaac 780
 aaatcttgc actataaattc caagcatcat aactctgaaa tatggaaact taaaggaaaa 840
 aaaagcccta ttttggagg acattgcaac ctatggagat gcatttttt ttctgccagc 900
 attttccttc agggccaaca cgggtacctc tttcaaagta tactacacgc tcgaagagtc 960
 taaagcaaga caaaaggttc tattttcca tcccaagttac ctgaaagatc tgcccttt 1020
 ctggagaact aaaggtgtga ctgcataccg cttgtccacc ggcttgcgttgc tcacaagtgt 1080
 tgcagtggaa ctgtgtaaaa atgtgaagct gtatggattc tggcccttct ctaaaactgt 1140
 agaagacata cctgtcagcc atcactattt tgacaacaag ctacctaaac atggtttcca 1200

tcagatgcc aaagaataca gccagatcct ccaacttcac atgaaaggaa tcctcaaact 1260
 gcaatttagc aaatgtgaag tcgcctaaac aaagtatctt aaaatggaa taattttaat 1320
 ataatgcagt aggtgattaa caatgtctcc aaacacccaa ggaggtggct aaagagtatt 1380
 ttgagatgag ccccaaaatt tggtttgacc aaagcttccc cactcattt gcaatgatgg 1440
 caagtcatc aatccttctc atcttcattt tttctcccta taacatggac accatatctg 1500

<210> 5
 <211> 529
 <212> PRT
 <213> Human

<400> 5

Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile
 1 5 10 15

Phe Ala Trp Gly Leu Leu Phe Leu Leu Ile Phe Ile Tyr Phe Thr Asp
 20 25 30

Ser Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr
 35 40 45

Arg Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala
 50 55 60

Ala His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu
 65 70 75 80

Pro Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu
 85 90 95

Gln Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe
 100 105 110

Ser Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp
 115 120 125

Asp Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr
130 135 140

Gln Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu
145 150 155 160

Gly Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg
165 170 175

His Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly
180 185 190

Asp Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp
195 200 205

Lys Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala
210 215 220

Met Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly
225 230 235 240

Lys Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg
245 250 255

Ser Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser
260 265 270

Ala Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu
275 280 285

His Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala
290 295 300

Ile Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val
305 310 315 320

Leu Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly
325 330 335

Asn Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro
340 345 350

Ser His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val
355 360 365

Ala Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys
370 375 380

Lys Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg
385 390 395 400

Asn Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln
405 410 415

Leu Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn
420 425 430

Pro Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys
435 440 445

Arg Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu
450 455 460

Leu Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly
465 470 475 480

Ala Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn
485 490 495

Met Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro
500 505 510

Gly Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His
 515 520 525

Ser

<210> 6
 <211> 1800
 <212> DNA
 <213> Human

<400> 6						
ggcgccggga ctccctcctg	gccgcccaca	gcctgtgcgc	attcctgcac	tcctgcccgc	60	
gcccgggacc	cgagccccc	gaggtgtcca	ggcgcggtgc	caggcgggta	ctgtgcaggt	120
tcattctgcc	accatctgc	attaagacac	aaggtgctga	ccgcagagac	ctgccatgaa	180
accacacttg	aagcaatgga	gacaacgaat	gctttcgga	atattcgctt	gggggctcct	240
cttttgctg	atttcatct	acttcaccga	cagcaacccc	gctgagcctg	tacccagctc	300
cctctccttc	ctggagacca	ggaggctcct	gccggtgcag	ggaaagcagc	ggccatcat	360
ggcgccgc	catgagccct	ccccgcctgg	gggcctggac	gcacgcccagg	cgctgcccgg	420
cggccaccca	gccggttcct	ttcatgcggg	gcctggagac	ctgcagaaat	gggcccagtc	480
ccaagatggg	tttgaacata	aagagttttt	ttcatcccag	gtggggagaa	aatctcaaag	540
tgctttctac	ccggaggatg	acgactactt	tttgctgct	ggtcagccag	ggtggcacag	600
ccacactcag	gggacattgg	attcccttc	ccccggggag	ccaggcccac	gggagggggc	660
ttttccggct	gcacaggtcc	agaggaggcg	ggtgaagaag	aggcaccgga	ggcagagaag	720
gagccacgtg	ttggaggagg	gacgacgacgg	cgacaggctg	tactcctcca	tgtccagggc	780
cttcctgtac	cggctctgga	aggggaacgt	ctcttccaaa	atgctgaacc	cgccgcctgca	840
gaaggcgatg	aaggattacc	tgaccgccaa	caagcacggg	gtgcgcttcc	gcgggaagcg	900
ggaggccggg	ctgagcaggg	cacagctgct	gtgccagctg	cgagccgcg	cgccgcgtgcg	960
gacgctggac	ggcaccgagg	cgccctttc	tgcgctgggc	tggcggcgcc	tgtgcccgc	1020
cgtccccctg	agccagctgc	accccccgg	cctgcgcagc	tgcgctgtcg	tcatgtctgc	1080

aggcgcaatc	ctcaactctt	ccttgggcga	ggaaatagat	tctcatgatg	cggtttgag	1140
attnaactct	gctcctacac	gtggttatga	gaaagatgtt	ggaaataaaa	ccaccatacg	1200
catcattaat	tcgcagattc	tgaccaaccc	cagccatcac	ttcattgaca	gttcactgta	1260
taaagacgtc	atttggtgg	cctgggaccc	tgccccatat	tccgcaaatc	ttaacctgtg	1320
gtacaaaaaa	ccggattaca	acctgttcac	tccatatatt	cagcatcgta	agagaaaccc	1380
aaatcagcca	ttttacattc	ttcatcctaa	atttatatgg	cagctctggg	atattatcca	1440
ggagaacact	aaagagaaga	ttcaacccaa	cccaccatct	tctggttca	ttggaatcct	1500
catcatgatg	tccatgtgca	gagaggtgca	cgtgtatgaa	tatatccat	ccgtgcggca	1560
gacggagctg	tgccactacc	acgagctgta	ctacgacgca	gcctgcaccc	tcggggcgta	1620
ccacccacta	ctctatgaga	agtcctggt	gcagcgctg	aacatggca	cgcaggggga	1680
tttgcatcgc	aaggcaagg	tggttcttcc	tggcttccag	gcggtgcact	gccctgcacc	1740
aagtccagtc	attccacact	ctaaaaagg	gtttcttggg	aatcaatgtg	caatggtaca	1800

<210> 7
 <211> 524
 <212> PRT
 <213> Mouse

 <400> 7

Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile
 1 5 10 15

Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn
 20 25 30

Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser
 35 40 45

Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala
 50 55 60

Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu
65 70 75 80

Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro
85 90 95

Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe
100 105 110

Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu
115 120 125

Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His
130 135 140

Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg
145 150 155 160

Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly
165 170 175

Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met
180 185 190

Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser Lys
195 200 205

Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser Phe
210 215 220

Asn Lys His Gly Val Arg Phe Arg Arg Arg Gly Arg Arg Glu Ala Thr
225 230 235 240

Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg Val
245 250 255

Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp Arg

260

265

270

Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly Leu
275 280 285

Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser Ser
290 295 300

Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn Ser
305 310 315 320

Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr Val
325 330 335

Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe Ile
340 345 350

Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro Ala
355 360 365

Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr Asn
370 375 380

Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln Pro
385 390 395 400

Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile Ile
405 410 415

Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly
420 425 430

Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His Val
435 440 445

Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr His
450 455 460

Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro Leu
 465 470 475 480

Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln Ala
 485 490 495

Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu
 500 505 510

Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser
 515 520

<210> 8
 <211> 1611
 <212> DNA
 <213> Mouse

<400> 8	60
caatgaaacc acacttgaag caatggcgac aacgaatgct ctttggaaata ttgtttggg	60
ggctcctctt ttggcaatt ttcatctact tcaccaacag caatcctgcg gcacctatgc	120
ccagctcctt ttccttcctg gagagccgtg ggctcctgcc tctacagggc aagcagcggg	180
tcatcatggg cgcttgcag gaaccctctt tgcccagaag ttggatgca agcaaagtgc	240
ttctggacag ccaccctgag aacccttcc acccttggcc tgggaccca cagaaatgg	300
atcaggcccc aaatggctt gacaatgggg atgagtttt tacatcccag gttggagga	360
aatcacaaag cgcttctat cccgaggaag atagctattt tttgttgcg gatcagcctg	420
agttgtacca ccacagggcag ggtgcactgg agctgccatc tccaggggag acatcatggc	480
gatcaggacc tgttcagccc aagcagaagc tgttcaccc aaggcgaggc agttgcctg	540
aggaagccta tgacagcgac atgctgtcag cctccatgtc gagagccttc ctgtaccggc	600
tctggaaggg ggcgtgtcc tctaagatgt tgaacccgcg cctgcagaag gccatgcgtt	660
actacatgtc cttcaacaag catggtgtgc gttccgcag gcggggtcgg cgtgaagcta	720
cacgtacagg gccggagctg ctgtgtgaga tgcgagacg tgtgcgtgtg cgcacgttgg	780

acggcagaga	ggcgcccttc	tcggggctgg	gctggcggcc	tctggtagcca	ggtgtacctc	840	
tgagccagtt	gcacccgcgc	ggtctgagca	gctgcgcagt	tgtcatgtct	gccgggtgc	900	
tcctgaactc	ctccttgggg	gaggaaatcg	attctcatga	tgcagtttg	agatttaact	960	
ctgcccctac	ccgtggctac	gagaaagatg	tcggaaataa	aaccacagta	cgcacatcatta	1020	
attctcagat	tctggccaac	cccagccatc	acttcattga	cagtgc	ttaaccttataaagatg	1080	
ttatcctgg	agcctggat	cctgctc	attctgcca	tcttaacctg	tggtaaaga	1140	
agccagatta	caac	tttc	actccatata	tccagcatcg	ccggaaatac	1200	
cattttacat	tcttcacccc	aagttcatat	ggcagcttg	ggacattatc	caggagaata	1260	
caagggagaa	gatacagccc	aacccaccat	cttctgg	tattgaaatc	ctcatcatga	1320	
tgtccatgt	taaagaggtg	cacgtgtatg	agtacatccc	atctgttcga	cagacagagc	1380	
tttgc	ccatgagctg	tactacgacg	cagcctgcac	cttgggg	taccacccac	1440	
tgctctatga	aaagctactg	gtgcagcgcc	ttaacacagg	cacccaggca	gacttgcatc	1500	
acaaggc	aa	ggtagtcttgc	ccaggcttcc	agaccctcg	gtgtccagta	accagcccc	1560
acaatacaca	ttctt	aaaat	ggaactcttgc	ggaactgatg	tgcaataagg	t	1611

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 9
 ctttctgga gaactaaagg

20

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 10
aattgcagtt tgaggattcc

20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 11
tggctcagga tgagatcggg

20

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 12
tactagcgct ccctgtgatt gg

22

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 13
tgctctcgag cccagccgac ggcgcctgccc

30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

14
tattctcgag ctaagaaacg ttaagccgtt 30

15
30
DNA
Artificial Sequence

15
Synthetic DNA

15
caattgacat atctgaatga gaagtcgctc 30

16
22
DNA
Artificial Sequence

16
Synthetic DNA

16
tactaacatc tcctgtggtt gg 22

17
20
DNA
Artificial Sequence

17
Synthetic DNA

17
ccagtgtccc agcctttgt 20

18
20
DNA
Artificial Sequence

18
Synthetic DNA

18

tgagtgggaa agctttggtc

20

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 19
gacaatgggg atgagtttt tacatccag

30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 20
cgatttcctc ccccaaggag gagttcagg

29

<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 21
acgttggacg gcagagaggc gcccttctcg

30

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 22
accttattgc acatcagttc ccaagagttc

30

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 23
caatgaaacc acacttgaag caatggcgac 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 24
cgcaacaaaa aaatagctat cttcctcggg 30

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 25
tcatctactt cacctcgagc aaccccgctg 30

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 26
catccaattg accaacagca atcctgcggc 30

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 27
ttatgattca caccaacctg aag 23

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 28
ctttgtactt gttcatgctt agg 23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 29
agacgtcatt ttgggtggcct ggg 23

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 30
ttaagagtgt ggaatgactg g 21